



3379.1.ST25.txt
SEQUENCE LISTING

<110> Kulp, David C.
Siani-Rose, Michael A.
Williams, Alan J.
Harmon, Cyrus L.

<120> Nucleic Acids Encoding G Proteins Coupled Receptors

<130> 3379.1

<140> 10/038,895

<141> 2001-10-24

<150> US 60/244,082

<151> 2000-10-26

<160> 20

<170> PatentIn version 3.2

<210> 1

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Organism

<220>

<221> misc_feature

<222> (126)..(126)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (146)..(146)

<223> Xaa can be any naturally occurring amino acid

<400> 1

Leu Leu Ala Pro Thr Gly Ser Leu Phe Arg Asn Cys Thr Gln Asp Gly
1 5 10 15

Trp Ser Glu Thr Phe Pro Arg Pro Asn Leu Ala Cys Gly Val Asn Val
20 25 30

Asn Asp Ser Ser Asn Glu Lys Arg Ser Tyr Leu Leu Lys Leu Lys Val
35 40 45

Met Tyr Thr Val Gly Tyr Ser Ser Ser Leu Val Met Leu Leu Val Ala
50 55 60

Leu Gly Ile Leu Cys Ala Phe Arg Arg Leu His Cys Thr Arg Asn Tyr
65 70 75 80

Ile His Met His Leu Phe Val Ser Phe Ile Leu Arg Ala Leu Ser Asn
Page 1

Phe Ile Lys Asp Ala Val Leu Phe Ser Ser Asp Asp Val Thr Tyr Cys
100 105 110

Asp Ala His Arg Gly Cys Lys Leu Val Met Val Leu Phe Xaa Tyr Cys
115 120 125

Ile Met Ala Asn Tyr Ser Trp Leu Leu Val Glu Gly Ser Thr Phe Thr
130 135 140

His Xaa Leu Ala Ile Ser Phe Phe Ser Glu Arg Lys Tyr Leu Gln Gly
145 150 155 160

Phe Val Ala Phe Gly Trp Gly Ser Pro Ala Ile Phe Val Ala Leu Trp
165 170 175

Ala Ile Ala Arg His Phe Leu Glu Asp Val Gly Cys Trp Asp Ile Asn
180 185 190

Ala Asn Ala Ser Ile Trp Trp Ile Ile Arg Gly Pro Val Ile Leu Ser
195 200 205

Ile Leu Asn Phe Ile Leu Phe Ile Asn Ile Leu Arg Ile Leu Met Arg
210 215 220

Lys Leu Arg Thr Gln Glu Thr Arg Gly Asn Glu Val Ser His Tyr Lys
225 230 235 240

Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His
245 250 255

Tyr Ile Val Phe Ala Phe Ser Pro Glu Asp Ala Met Glu Ile Gln Leu
260 265 270

Phe Phe

<210> 2
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 2
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ttccccaggc ctaatctggc ctgtggcggtt aatgtgaacg actcttccaa cgagaagcgg 120
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cactcctacc tgctgaagct gaaagtcatg tacaccgtgg gctacagctc ctccctggtc 180
atgctcctgg tcgcccttgg catcctctgt gctttccgga ggctccactg cactcgcaac 240
tacatccaca tgcacctgtt cgtgtccttc atccttcgtg cctgttccaa cttcatcaag 300
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aagctgggtca tgggtgctgtt c 381

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<210> 3
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<220>
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<220>
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<222> (58)..(58)
<223> n is a, c, g, or t

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ggttctccag ccatttttgt tgctttgtgg gctattgcc a gacactttct ggaagatgtt 180
gggtgctggg acatcaatgc caacgcatcc atctggtgga tcattcgtgg tcctgtgatc 240
ctctccatcc tgattaattt catccttttc ataaacattc taagaatcct gatgagaaaa 300
cttagaacc c aagaacaag aggaaatgaa gtcagccatt ataagcgctt ggccaggtcc 360
actctctgc tgatccccct ctttggcatc cactacatcg tcttcgcctt ctccccagag 420
gacgctatgg agatccagct gtttttt 447

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<210> 4
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<220>
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<220>
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<222> (439)..(439)
<223> n is a, c, g, or t

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ttccccaggc ctaatctggc ctgtggcggt aatgtgaacg actcttccaa cgagaagcgg 120

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tacatccaca tgcacctgtt cgtgtccttc atccttcgtg cctgttccaa ctcatcaag 300
gacgccgtgc tcttctcctc agatgatgtc acctactgcg atgcccacag ggcgggctgc 360
aagctgggtca tgggtgctgtt ctactgcac atggccaact actcctggct gctgggtggaa 420
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agacactttc tgggaagatgt tgggtgctgg gacatcaatg ccaacgcac catctgggtg 600
atcattcgtg gtcctgtgat cctctccatc ctgattaatt tcacctttt cataaacatt 660
ctaagaatcc tgatgagaaa acttagaacc caagaaacaa gaggaatga agtcagccat 720
tataagcgcc tggccaggtc cactctcctg ctgatcccc tctttggcat ccactacatc 780
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<210> 5
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Organism

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Pro Thr Phe Ile Leu Phe Ser Phe Gln Pro Gly Asp Lys Arg Thr Lys
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His Ile Cys Val Tyr Trp Glu Gly Ser Glu Gly Gly His Trp Ser Thr
 20 25 30

Glu Gly Cys Ser His Val His Ser Asn Gly Ser Tyr Thr Lys Cys Lys
 35 40 45

Cys Phe His Leu Ser Ser Phe Ala Val Leu Val Ala Leu Ala Pro Lys
 50 55 60

Asp Pro Val Leu Thr Val Ile Thr Gln Val Gly Leu Thr Ile Ser Leu
 65 70 75 80

Leu Cys Leu Phe Leu Ala Ile Leu Thr Phe Leu Leu Cys Arg Pro Ile
 85 90 95

Gln Asn Thr Ser Thr Ser Leu His Leu Glu Leu Ser Leu Cys Leu Phe
 100 105 110

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Leu Ala His Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Glu Pro Glu
 115 120 125

Leu Cys Ser Ile Ile Ala Gly Leu Leu His Phe Leu Tyr Leu Ala Cys
 130 135 140

Phe Thr Trp Met Leu Leu Glu Gly Leu His Leu Phe Leu Thr Val Arg
 145 150 155 160

Asn Leu Lys Val Ala Asn Tyr Thr Ser Thr Gly Arg Phe Lys Lys Arg
 165 170 175

Phe Met Tyr Pro Val Gly Tyr Gly Ile Pro Ala Val Ile Ile Ala Val
 180 185 190

Ser Ala Ile Val Gly Pro Gln Asn Tyr Gly Thr Phe Thr His Cys Trp
 195 200 205

Leu Lys Leu Asp Lys Gly Phe Ile Trp Ser Phe Met Gly Pro Val Ala
 210 215 220

Val Ile Ile Leu Asn Leu Val Phe Tyr Phe Gln Val Leu Trp Ile Leu
 225 230 235 240

Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser Thr Ile Gln Asp
 245 250 255

Thr Arg Val Met Thr Phe Lys Ala Ile Ser Gln Leu Phe Ile Leu Gly
 260 265 270

Cys Ser Trp Gly Leu Gly Phe Phe Met Val Glu Glu Val Gly Lys Thr
 275 280 285

Ile Gly Ser Ile Ile Ala Tyr Ser Phe Thr Ile Ile Asn Thr Leu Gln
 290 295 300

Gly Val Leu Leu Phe Val Val His Cys Leu Leu Asn Arg Gln Val Arg
 305 310 315 320

<210> 6
 <211> 969
 <212> DNA
 <213> Artificial Sequence

<220>
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 cttgccccca aggaggaccc tgtgtgacc gtgatcacc aggtggggct gaccatctct 240
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 agcacctccc tccatctaga gctctccctc tgcctcttcc tggcccacct cctgttcctg 360
 acgggcatca acagaactga gcctgaggtg ctgtgtcca tcattgcagg gctgtgtcac 420
 ttctctacc tggcttgctt cacctggatg ctctggaag ggctgcacct cttcctcacc 480
 gtcaggaacc tcaaggtggc caactacacc agcacgggca gattcaagaa gaggttcatg 540
 taccctgtag gctacgggat cccagctgtg attattgtg tgtcagcaat agttggaccc 600
 cagaattatg gaacatttac tctgtttgg ctcaagcttg ataaaggatt catctggagc 660
 ttcatggggc cagtagcagt cattatcttg ataaacctgg tgttctactt ccaagttctg 720
 tggattttga gaagcaaact ttctccctc aataaagaag tttccaccat tcaggacacc 780
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 ggttttttta tggttgaaga agtagggaag acgattggat caatcattgc atactcattc 900
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<210> 7
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Organism

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Gln His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr Trp
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Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe Thr
 20 25 30

Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys
 35 40 45

Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile Gly
 50 55 60

Ile Asn Arg Thr Asp Gln Pro Ala Cys Ala Val Phe Ala Ala Leu Leu
 65 70 75 80

His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu Gly Val
 85 90 95

Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His Ser Arg
 100 105 110

Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu Ile Val
 115 120 125

Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp Lys Val
 130 135 140

Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe Ile Gly Pro
 145 150 155 160

Ala Thr Leu Ile Ile Met Asn Val Ile Phe Leu Gly Ile Ala Leu Tyr
 165 170 175

Lys Met Phe His His Thr Ala Ile Leu Lys Pro Glu Ser Gly Cys Leu
 180 185 190

Asp Asn Ile Lys Leu Lys Ile Asn Ile Pro Ile Ile Lys Ser Ile Tyr
 195 200 205

Ile Tyr Met Tyr Ile Cys Met Cys Val
 210 215

<210> 8
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<220>
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 agtgaccgta acaccatcca caagaacctc tgcattcagtc tctttgtagc agagctgctc 180
 ttcttgattg ggatcaaccg aactgaccaa ccaattgcct gtgctgtttt cgctgccctg 240
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 atcatgctgg tggagggttt tgagagtga cattcacgta ggaaatactt ttatctggct 360
 ggctatggga tgcctgcact cattgtggct gtgtcagctg cagtagacta caggagttat 420
 ggaacagata aagtatgttg gctccgactt gacacctact tcatttggag ttttatagga 480
 ccagcaactt tgataattat gcttaatgta atcttccttg ggattgcttt atataaaatg 540

tttcatcata ctgctataact gaaacctgaa tcaggctgtc ttgataacat caagttaaaa 600

attaatatcc caattataaa atctatttat atctatatgt atatatgcat gtgtgtg 657

<210> 9
 <211> 304
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Organism

<400> 9

Gly Asn Val Ala Val Ala Phe Val Tyr Tyr Lys Ser Ile Gly Pro Leu
 1 5 10 15

Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln Asn Tyr Asp Asn
 20 25 30

Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile Ser Val Ser Met
 35 40 45

Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys Ile Thr Phe Thr
 50 55 60

Leu Ser His Arg Lys Thr Asp Arg Tyr Arg Ser Leu Cys Ala Phe Trp
 65 70 75 80

Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser Glu Gly Cys
 85 90 95

Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser Cys Arg Cys Asn His
 100 105 110

Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser Ile Ile Lys
 115 120 125

Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly Ile Ile Ile Ser
 130 135 140

Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp Phe Phe Ser Glu
 145 150 155 160

Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn Leu Cys Cys Ser Leu
 165 170 175

Phe Leu Ala Glu Leu Val Phe Leu Val Gly Ile Asn Thr Asn Thr Asn
 180 185 190

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Lys Phe Cys Ser Ile Ile Ala Gly Leu Leu His Tyr Phe Phe Leu Ala
 195 200 205

Ala Phe Ala Trp Met Cys Ile Glu Gly Ile His Leu Tyr Leu Ile Val
 210 215 220

Val Gly Val Ile Tyr Asn Lys Gly Phe Leu His Lys Asn Phe Tyr Ile
 225 230 235 240

Phe Gly Tyr Leu Ser Pro Ala Val Val Val Gly Phe Ser Ala Ala Leu
 245 250 255

Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys Val Cys Trp Leu Ser Thr Glu
 260 265 270

Asn Asn Phe Ile Trp Ser Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu
 275 280 285

Val Cys Ile Tyr Lys Ile Val Ile Thr Ile Gln Lys Ser Asp Asp His
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 <211> 921
 <212> DNA
 <213> Artificial Sequence

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 tcttcagtaa tttcagtctc aatgagctca aaccacacca cattatatga acttgaaaaa 180
 ataacattta cattaagtca tcgaaaggct acagataggt ataggagtct atgtgcattt 240
 tggaattact cacctgatac catgaatggc agctggctct cagagggctg tgagctgaca 300
 tactcaaatg agaccacac ctcatgccgc tgtaatcacc tgacacattt tgcaattttg 360
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 attgccggac tgctacacta cttcttttta gctgcttttg catggatgtg cattgaaggc 660
 atacatctct atctcattgt tgtgggtgtc atctacaaca agggattttt gcacaagaat 720
 ttttatatct ttggctatct aagcccagcc gtggtagttg gattttcggc agcactagga 780

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 agttttatag gaccagcatg cctaatacatt cttgtatgta tatataaaat tgttattaca 900
 attcaaaaaa gtgatgatca t 921

<210> 11
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 <212> PRT
 <213> Artificial Sequence

<220>
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Ser Thr Ala Cys Phe Cys Asn His Ser Thr Ser Phe Ala Ile Leu Leu
 20 25 30

Gln Ile Tyr Glu Val Gln Gly Pro Glu Glu Glu Ser Leu Leu Arg Thr
 35 40 45

Leu Ser Phe Val Gly Cys Gly Val Ser Phe Cys Ala Leu Thr Thr Thr
 50 55 60

Phe Leu Leu Phe Leu Val Ala Gly Val Pro Lys Ser Glu Arg Thr Thr
 65 70 75 80

Val His Lys Asn Leu Thr Phe Ser Leu Ala Ser Ala Glu Gly Phe Leu
 85 90 95

Met Thr Ser Glu Trp Ala Lys Ala Asn Glu Ala Cys Val Ala Val Thr
 100 105 110

Val Ala Met His Phe Leu Phe Leu Val Ala Phe Ser Trp Met Leu Val
 115 120 125

Glu Gly Leu Leu Leu Trp Arg Lys Val Val Ala Val Ser Met His Pro
 130 135 140

Gly Pro Gly Met Arg Leu Tyr His Ala Thr Gly Trp Gly Val Pro Val
 145 150 155 160

Gly Ile Val Ala Val Thr Leu Ala Met Leu Pro His Asp Tyr Val Ala
 165 170 175

Pro Gly His Cys Trp Leu Asn Val His Thr Asn Ala Ile Trp Ala Phe
 180 185 190

Val Gly Pro Val Leu Phe Val Leu Thr Val Ser
195 200

<210> 12
<211> 615
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<213> Artificial Sequence

<220>
<223> Synthetic Organism

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cctgaggagg agtcgctgct gaggactctg tcatttggtg gctgtggcgt gtccttctgc 180
gccctcacca ccaccttctt gctcttcctg gtggccgggg tccccaagtc agagcgaacc 240
acagtccaca agaacctcac cttctccctg gcctctgccg agggcttcct catgaccagc 300
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gtgctgactg tgagc 615

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<212> PRT
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<220>
<223> Synthetic Organism

<400> 13

Met Lys Ser Pro Arg Arg Thr Thr Leu Cys Leu Met Phe Ile Val Ile
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Tyr Ser Ser Lys Ala Ala Leu Asn Trp Asn Tyr Glu Ser Thr Ile His
20 25 30

Pro Leu Leu His Glu His Glu Pro Ala Gly Glu Glu Ala Leu Arg Gln
35 40 45

Lys Arg Ala Val Ala Thr Lys Ser Pro Thr Ala Glu Glu Tyr Thr Val
50 55 60

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Asn Ile Glu Ile Ser Phe Glu Asn Ala Ser Phe Leu Asp Pro Ile Lys
65 70 75 80

Ala Tyr Leu Asn Ser Leu Ser Phe Pro Ile His Gly Asn Asn Thr Asp
85 90 95

Gln Ile Thr Asp Ile Leu Ser Ile Asn Val Thr Thr Val Cys Arg Pro
100 105 110

Ala Gly Asn Glu Ile Trp Cys Ser Cys Glu Thr Gly Tyr Gly Trp Pro
115 120 125

Arg Glu Arg Cys Leu His Asn Leu Ile Cys Gln Glu Arg Asp Val Phe
130 135 140

Leu Pro Gly His His Cys Ser Cys Leu Lys Glu Leu Pro Pro Asn Gly
145 150 155 160

Pro Phe Cys Leu Leu Gln Glu Asp Val Thr Leu Asn Met Arg Val Arg
165 170 175

Leu Asn Val Gly Phe Gln Glu Asp Leu Met Asn Thr Ser Ser Ala Leu
180 185 190

Tyr Arg Ser Tyr Lys Thr Asp Leu Glu Thr Ala Arg Lys Gly Tyr Gly
195 200 205

Ile Leu Pro Gly Phe Lys Gly Val Thr Val Thr Gly Phe Lys Ser Gly
210 215 220

Ser Val Val Val Thr Tyr Glu Val Lys Thr Thr Pro Pro Ser Leu Glu
225 230 235 240

Leu Ile His Lys Ala Asn Glu Gln Val Val Gln Ser Leu Asn Gln Thr
245 250 255

Tyr Lys Met Asp Tyr Asn Ser Phe Gln Ala Val Thr Ile Asn Glu Ser
260 265 270

Asn Phe Phe Val Thr Pro Glu Ile Ile Phe Glu Gly Asp Thr Val Ser
275 280 285

Leu Val Cys Glu Lys Glu Val Leu Ser Ser Asn Val Ser Trp Arg Tyr
290 295 300

Glu Glu Gln Gln Leu Glu Ile Gln Asn Ser Ser Arg Phe Ser Ile Tyr
305 310 315 320

3379.1.ST25.txt

Thr Ala Leu Phe Asn Asn Met Thr Ser Val Ser Lys Leu Thr Ile His
 325 330 335
 Asn Ile Thr Pro Gly Asp Ala Gly Glu Tyr Val Cys Lys Leu Ile Leu
 340 345 350
 Asp Ile Phe Glu Tyr Glu Cys Lys Lys Lys Ile Asp Val Met Pro Ile
 355 360 365
 Gln Ile Leu Ala Asn Glu Glu Met Lys Val Met Cys Asp Asn Asn Pro
 370 375 380
 Val Ser Leu Asn Cys Cys Ser Gln Gly Asn Val Asn Trp Ser Lys Val
 385 390 395 400
 Glu Trp Lys Gln Glu Gly Lys Ile Asn Ile Pro Gly Thr Pro Glu Thr
 405 410 415
 Asp Ile Asp Ser Ser Cys Ser Arg Tyr Thr Leu Lys Ala Asp Gly Thr
 420 425 430
 Gln Cys Pro Ser Gly Ser Ser Gly Thr Thr Val Ile Tyr Thr Cys Glu
 435 440 445
 Phe Ile Ser Ala Tyr Gly Ala Arg Gly Ser Ala Asn Ile Lys Val Thr
 450 455 460
 Phe Ile Ser Val Ala Asn Leu Thr Ile Thr Pro Asp Pro Ile Ser Val
 465 470 475 480
 Ser Glu Gly Gln Asn Phe Ser Ile Lys Cys Ile Ser Asp Val Ser Asn
 485 490 495
 Tyr Asp Glu Val Tyr Trp Asn Thr Ser Ala Gly Ile Lys Ile Tyr Gln
 500 505 510
 Arg Phe Tyr Thr Thr Arg Arg Tyr Leu Asp Gly Ala Glu Ser Val Leu
 515 520 525
 Thr Val Lys Thr Ser Thr Arg Glu Trp Asn Gly Thr Tyr His Cys Ile
 530 535 540
 Phe Arg Tyr Lys Asn Ser Tyr Ser Ile Ala Thr Lys Asp Val Ile Val
 545 550 555 560
 His Pro Leu Pro Leu Lys Leu Asn Ile Met Val Asp Pro Leu Glu Ala

Thr Val Ser Cys Ser Gly Ser His His Ile Lys Cys Cys Ile Glu Glu
580 585 590

Asp Gly Asp Tyr Lys Val Thr Phe His Thr Gly Ser Ser Ser Leu Pro
595 600 605

Ala Ala Lys Glu Val Asn Lys Lys Gln Val Cys Tyr Lys His Asn Phe
610 615 620

Asn Ala Ser Ser Val Ser Trp Cys Ser Lys Thr Val Asp Val Cys Cys
625 630 635 640

His Phe Thr Asn Ala Ala Asn Asn Ser Val Trp Ser Pro Ser Met Lys
645 650 655

Leu Asn Leu Val Pro Gly Glu Asn Ile Thr Cys Gln Asp Pro Val Ile
660 665 670

Gly Val Gly Glu Pro Gly Lys Val Ile Gln Lys Leu Cys Arg Phe Ser
675 680 685

Asn Val Pro Ser Ser Pro Glu Ser Pro Ile Gly Gly Thr Ile Thr Tyr
690 695 700

Lys Cys Val Gly Ser Gln Trp Glu Glu Lys Arg Asn Asp Cys Ile Ser
705 710 715 720

Ala Pro Ile Asn Ser Leu Leu Gln Met Ala Lys Leu Ile Lys Ser Pro
725 730 735

Ser Gln Asp Glu Met Leu Pro Thr Tyr Leu Lys Asp Leu Ser Ile Ser
740 745 750

Ile Asp Lys Ala Glu His Glu Ile Ser Ser Ser Pro Gly Ser Leu Gly
755 760 765

Ala Ile Ile Asn Ile Leu Asp Leu Leu Ser Thr Val Pro Thr Gln Val
770 775 780

Asn Ser Glu Met Met Thr Val Leu Ser Thr Val Asn Val Ile Leu Gly
785 790 795 800

Lys Pro Val Leu Asn Thr Trp Lys Val Leu Gln Gln Gln Trp Thr Asn
805 810 815

Gln Ser Ser Gln Leu Leu His Ser Val Glu Arg Phe Ser Gln Ala Leu
820 825 830

Gln Ser Gly Asp Ser Pro Pro Leu Ser Phe Ser Gln Thr Asn Val Gln
835 840 845

Met Ser Ser Met Val Ile Lys Ser Ser His Pro Glu Thr Tyr Gln Gln
850 855 860

Arg Phe Val Phe Pro Tyr Phe Asp Leu Trp Gly Asn Val Val Ile Asp
865 870 875 880

Lys Ser Tyr Leu Glu Asn Leu Gln Ser Asp Ser Ser Ile Val Thr Met
885 890 895

Ala Phe Pro Thr Leu Gln Ala Ile Leu Ala Gln Asp Ile Gln Glu Asn
900 905 910

Asn Phe Ala Glu Ser Leu Val Met Thr Thr Thr Val Ser His Asn Thr
915 920 925

Thr Met Pro Phe Arg Ile Ser Met Thr Phe Lys Asn Asn Ser Pro Ser
930 935 940

Gly Gly Glu Thr Lys Cys Val Phe Trp Asn Phe Arg Leu Ala Asn Asn
945 950 955 960

Thr Gly Gly Trp Asp Ser Ser Gly Cys Tyr Val Glu Glu Gly Asp Gly
965 970 975

Asp Asn Val Thr Cys Ile Cys Asp His Leu Thr Ser Phe Ser Ile Leu
980 985 990

Met Ser Pro Asp Ser Pro Asp Pro Ser Ser Leu Leu Gly Ile Leu Leu
995 1000 1005

Asp Ile Ile Ser Tyr Val Gly Val Gly Phe Ser Ile Leu Ser Leu
1010 1015 1020

Ala Ala Cys Leu Val Val Glu Ala Val Val Trp Lys Ser Val Thr
1025 1030 1035

Lys Asn Arg Thr Ser Tyr Met Arg His Thr Cys Ile Val Asn Ile
1040 1045 1050

Ala Ala Ser Leu Leu Val Ala Asn Thr Trp Phe Ile Val Val Ala
1055 1060 1065

3379.1.ST25.txt

Ala Ile Gln Asp Asn Arg Tyr Ile Leu Cys Lys Thr Ala Cys Val
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 Trp Met Leu Thr Leu Gly Leu Met Leu Phe Tyr Arg Leu Val Phe
 1100 1105 1110
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 1115 1120 1125
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 Gly Ala Thr Gln Pro Arg Glu Val Tyr Thr Arg Lys Asn Val Cys
 1145 1150 1155
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 1160 1165 1170
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 1235 1240 1245
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3379.1.ST25.txt

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Asn

<210> 14
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3379.1.ST25.txt

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3379.1.ST25.txt

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<220>
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<400> 15

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Asn Ser Ser Tyr Ile Leu Leu His Ser Val Asn Ser Phe Ala Arg Arg
20           25           30

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Leu Phe Ile Asp Asn Ile Pro Val Asp Ile Ser Asp Val Phe Ile His
35           40           45

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Thr Met Gly Thr Thr Ile Ser Gly Asp Asn Ile Gly Lys Asn Phe Thr
50           55           60

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Phe Ser Met Arg Ile Asn Asp Thr Ser Asn Glu Val Thr Gly Arg Val
65           70           75           80

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3379.1.ST25.txt

Leu Ile Ser Arg Asp Glu Leu Arg Lys Val Pro Ser Pro Ser Gln Val
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 115 120 125
 Lys Glu Leu Lys Arg Ile Ser Leu Ile Phe Glu Lys Ile Ser Lys Ser
 130 135 140
 Glu Glu Arg Arg Thr Gln Cys Val Gly Trp His Ser Val Glu Asn Arg
 145 150 155 160
 Trp Asp Gln Gln Ala Cys Lys Met Ile Gln Glu Asn Ser Gln Gln Ala
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 Val Cys Lys Cys Arg Pro Ser Lys Leu Phe Thr Ser Phe Ser Ile Leu
 180 185 190
 Met Ser Pro His Ile Leu Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr
 195 200 205
 Val Gly Leu Gly Ile Ser Ile Cys Ser Leu Ile Leu Cys Leu Ser Ile
 210 215 220
 Glu Val Leu Val Trp Ser Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu
 225 230 235 240
 Arg His Val Cys Ile Val Asn Ile Ala Ala Thr Leu Leu Met Ala Asp
 245 250 255
 Val Trp Phe Ile Val Ala Ser Phe Leu Ser Gly Pro Ile Thr His His
 260 265 270
 Lys Gly Cys Val Ala Ala Thr Phe Phe Val His Phe Phe Tyr Leu Ser
 275 280 285
 Val Phe Phe Trp Met Leu Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile
 290 295 300
 Met Ile Val Phe His Thr Leu Pro Lys Ser Val Leu Val Ala Ser Leu
 305 310 315 320
 Phe Ser Val Gly Tyr Gly Cys Pro Leu Ala Ile Ala Ala Ile Thr Val
 325 330 335

Ala Ala Thr Glu Pro Gly Lys Gly Tyr Leu Arg Pro Glu Ile Cys Trp
 340 345 350

Leu Asn Trp Asp Met Thr Lys Ala Leu Leu Ala Phe Val Ile Pro Ala
 355 360 365

Leu Ala Ile Val Val Val Asn Leu Ile Thr Val Thr Leu Val Ile Val
 370 375 380

Lys Thr Gln Arg Ala Ala Ile Gly Asn Ser Met Phe Gln Glu Val Arg
 385 390 395 400

Ala Ile Val Arg Ile Ser Lys Asn Ile Ala Ile Leu Thr Pro Leu Leu
 405 410 415

Gly Leu Thr Trp Gly Phe Gly Val Ala Thr Val Ile Asp Asp Arg Ser
 420 425 430

Leu Ala Phe His Ile Ile Phe Ser Leu Leu Asn Ala Phe Gln Phe Phe
 435 440 445

Ile Leu Val Phe Gly Thr Ile Leu Asp Pro Lys Val
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 aaaaatttca ctttttctat gagaattaat gacaccagca atgaagtcac tgggagagtg 240
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 atcagcaagt cagaggagag gaggacacag tgtgttggct ggcactctgt ggagaacaga 480
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3379.1.ST25.txt

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 20 25 30

Leu Leu Pro Thr Leu Asp Gln Ser Thr Val His Ile Leu Thr Arg Ile
 35 40 45

Ser Gln Ala Gly Cys Gly Val Ser Met Ile Phe Leu Ala Phe Thr Ile
 50 55 60

Ile Leu Tyr Ala Phe Leu Arg Leu Ser Arg Glu Arg Phe Lys Ser Glu
 65 70 75 80

Asp Ala Pro Lys Ile His Val Ala Leu Gly Gly Ser Leu Phe Leu Leu
 85 90 95

3379.1.ST25.txt

Asn Leu Ala Phe Leu Val Asn Val Gly Ser Gly Ser Lys Gly Ser Asp
100 105 110

Ala Ala Cys Trp Ala Arg Gly Ala Val Phe His Tyr Phe Leu Leu Cys
115 120 125

Ala Phe Thr Trp Met Gly Leu Glu Ala Phe His Leu Tyr Leu Leu Ala
130 135 140

Val Arg Val Phe Asn Thr Tyr Phe Gly His Tyr Phe Leu Lys Leu Ser
145 150 155 160

Leu Val Gly Trp Gly Leu Pro Ala Leu Met Val Ile Gly Thr Gly Ser
165 170 175

Ala Asn Ser Tyr Gly Leu Tyr Thr Ile Arg Asp Arg Glu Asn Arg Thr
180 185 190

Ser Leu Glu Leu Cys Trp Phe Arg Glu Gly Thr Thr Met Tyr Ala Leu
195 200 205

Tyr Ile Thr Val His Gly Tyr Phe Leu Ile Thr Phe Leu Phe Gly Met
210 215 220

Val Val Leu Ala Leu Val Val Trp Lys Ile Phe Thr Leu Ser Arg Ala
225 230 235 240

Thr Ala Val Lys Glu Arg Gly Lys Asn Arg Lys Lys Val Leu Thr Leu
245 250 255

Leu Gly Leu Ser Ser Leu Val Gly Val Thr Trp Gly Leu Ala Ile Phe
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60

3379.1.ST25.txt

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<220>
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<400> 19

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Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn Leu Phe Ala
 20 25 30

Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val Asn Glu Leu
 35 40 45

Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr Ser Glu Lys
 50 55 60

Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu Asp Ile Leu
 65 70 75 80

Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu Trp Pro Asn
85 90 95

Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly Ala Ile Leu
100 105 110

Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln Val Asn Gly
115 120 125

Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu Ile Ile Leu
130 135 140

Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala Gln Cys Val
145 150 155 160

Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu Lys Ala Cys Gln Met
165 170 175

Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn Tyr Thr Ser
180 185 190

Val Val Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser Met Thr Asp
195 200 205

Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu Ser Val Ser Ile Leu
210 215 220

Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr Val Trp Ser Arg Val
225 230 235 240

Val Val Thr Glu Ile Ser Tyr Met Arg His Val Cys Ile Val Asn Ile
245 250 255

Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe Ile Ile Gly Ser His
260 265 270

Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys Val Ala Val Thr Phe
275 280 285

Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe Trp Met Leu Phe Lys
290 295 300

Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile Phe Arg Arg Met Met
305 310 315 320

Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile Gly Tyr Gly Cys Pro
Page 25

Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr Glu Pro Glu Lys Gly
340 345 350

Tyr Ile Arg Pro Glu Ala Cys Trp Leu Asn Trp Asp Asn Thr Lys Ala
355 360 365

Leu Xaa Ala Phe Ala Ile Pro Ala Phe Val Ile Val Ala Val Asn Leu
370 375 380

Ile Val Val Leu Val Val Ala Val Asn Thr Gln Arg Pro Ser Ile Gly
385 390 395 400

Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile Ser Lys Asn
405 410 415

Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly Phe Gly Ile
420 425 430

Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile Ile Phe Ala
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Asp His Lys Val
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3379.1.ST25.txt

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